

SEQUENCE LISTING

<110> Presnell, Scott R.
Kindsvogel, Wayne

<120> NOVEL CYTOKINE ZCYT018

<130> 99-106C1

<150> US 60/172,105

<151> 1999-12-23

<150> US 60/250,841

<151> 2000-12-01

<150> US 09/746,375

<151> 2000-12-22

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<213> Homo sapiens

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Leu Met Gly Thr	Leu Ala Thr	Ser Cys Leu	Leu Leu Leu	Ala Leu Leu	
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gta cag gga gga	gca gct gcg	ccc atc agc	tcc cac tgc	agg ctt gac	149
Val Gln Gly Gly	Ala Ala Ala	Pro Ile Ser	Ser His Cys	Arg Leu Asp	

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Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu			
45	50	55	
gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att			245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile			
60	65	70	75
ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg			293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu			
80	85	90	
atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa			341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln			
95	100	105	
tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc			389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala			
110	115	120	
agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg			437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu			
125	130	135	
cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt			485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu			
140	145	150	155
gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt			533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe			
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Met Ser Leu Arg Asn Ala Cys Ile			
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tagttacaaa ggaaccaat gccacttttg tttataagac cagaaggtag actttctaag			767
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tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa    1007
acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta    1067
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Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
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His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
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Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
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Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115          120          125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
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Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
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Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly			
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Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met			
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Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser			
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Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg			
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Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His			
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acnaaymgna cnttyatgyt ngcnaargar gcnwsnytny cngayaayaa yacngaygtn	180
mgnytnathg gngaraaryt nttycayggn gtnwsnatgw sngarmngtg ytayytnatg	240
aarcargtny tnaayttyac nytnygargar gtynynttyc cncarwsnga ymgnttycar	300
ccntayatgc argargtngt nccnttyytn gcnmgnytnw snaaymgnyt nwsnacntgy	360
cayathgarg gngaygayt ncayathcar mgnaaygtnc araarytnaa rgayacngtn	420
aaraarytng gngarwsngg ngarathaar gcnathggng arytnyayyt nytnttyatg	480

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<212> PRT

<213> Artificial Sequence

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<223> C-terminal FLAG peptide tag

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5

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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

10

15

20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150

Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

25

30

35

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Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

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Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys				
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cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac				294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn				
	75	80	85	
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc				342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly				
	90	95	100	
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act				390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr				
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acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att				438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile				
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Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly				
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cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta				534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu				
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gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag				582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln				
	170	175	180	
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc				630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly				
	185	190	195	
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac				678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr				
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atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc				726

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Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
			235					240					245			
tac	ctg	agc	tac	aga	tat	gtc	acc	aag	ccg	cct	gca	cct	ccc	aac	tcc	822
Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
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Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
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Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
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Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	
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Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala	
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Leu Thr Val Gln Trp Glu Ser
570

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Val	Gln	Pro	Ser	Ser	Tyr	Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro
385					390					395					400
Pro	Ser	Tyr	Gly	Val	Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr
				405					410					415	
Gly	Thr	Leu	Ser	Ser	Pro	Lys	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln
			420					425					430		

Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445

Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460

His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480

Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495

Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510

Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525

Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540

Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560

Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
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39

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37

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<210> 26
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<210> 29
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<400> 30
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<210> 31
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 <213> Homo sapiens

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 1 5 10 15

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln

35	40	45	
cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac			192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr			
50	55	60	
aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt			240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly			
65	70	75	80
act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag			288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln			
85	90	95	
gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca			336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser			
100	105	110	
gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata			384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile			
115	120	125	
gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta			432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val			
130	135	140	
att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat			480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn			
145	150	155	160
gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att			528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile			
165	170	175	
aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga			576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg			
180	185	190	
gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg			624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val			
195	200	205	
gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa			672

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttggtg aatttggtcat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtggt tgaaggatct tattttaaatt 783
 tgtttttgta ttttcttaaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatatatt gaacgacatt cccccgaaa 903
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 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagt ataaatggat 1983
 taaaaaatat tcagaaatgt attggggggt ggaggagaat aagaggcaga gcaagagcta 2043
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<213> Homo sapiens

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 20 25 30
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln

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      35              40              45
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
  50              55              60
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
  65              70              75              80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
      85              90              95
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
      100              105              110
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
      115              120              125
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
      130              135              140
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
      145              150              155              160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
      165              170              175
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
      180              185              190
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
      195              200              205
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
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Glu Arg Cys Val Glu Ile Pro
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<210> 34

<211> 29

<212> PRT

<213> Artificial Sequence

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<223> Human ZCYT018 peptide 1 (huZCYT018-1)

<400> 34

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Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys
      20              25

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<210> 35

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 2 (huZCYT018-2)

<400> 35

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Glu	Val	Val	Pro	Cys											
			20												

<210> 36

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Human ZCYT018 peptide 3 (huZCYT018-3)

<400> 36

Cys	Asn	Val	Gln	Lys	Leu	Lys	Asp	Thr	Val	Lys	Lys	Leu	Gly	Glu	Ser
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Gly	Glu	Ile	Lys	Ala	Ile	Gly	Glu								
			20												

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<211> 778

<212> DNA

<213> mus musculus

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<222> (47)...(583)

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						1		

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Leu	Gln	Lys	Ser	Met	Ser	Phe	Ser	Leu	Met	Gly	Thr	Leu	Ala	Ala	Ser	
5						10					15					

tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat gcg ctg ccc Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala Leu Pro 20 25 30 35	151
gtc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag cag ccg tac Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln Pro Tyr 40 45 50	199
atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc ctt gca gat Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu Ala Asp 55 60 65	247
aac aac aca gat gtc cgg ctc atc ggg gag aaa ctg ttc cga gga gtc Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg Gly Val 70 75 80	295
aat gct aag gat cag tgc tac ctg atg aag cag gtg ctc aac ttc acc Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn Phe Thr 85 90 95	343
ctg gaa gac gtt ctg ctc ccc cag tca gac agg ttc cag ccc tac atg Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met 100 105 110 115	391
cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag ctc agc tcc Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu Ser Ser 120 125 130	439
tgt cac atc agc ggt gac gac cag aac atc cag aag aat gtc aga agg Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val Arg Arg 135 140 145	487
ctg aag gag aca gtg aaa aag ctt gga gag agt gga gag atc aag gcg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala 150 155 160	535
att ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat gct tgc gtc Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Val 165 170 175	583
tgagcgagaa gaagctagaa aacgaagaac tgctccttcc tgccttctaa aaagaacaat aagatccctg aatggacttt ttactaaag gaaagtgaga agctaacgtc catcatcatt agaagatttc acatgaaacc tggctcagtt gaaaaagaaa atagtgtcaa gttgtccatg	643 703 763

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778

<210> 38

<211> 179

<212> PRT

<213> mus musculus

<400> 38

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Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
 35           40           45
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50           55           60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65           70           75           80
Arg Gly Val Asn Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
 85           90           95
Asn Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln
100          105          110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
115          120          125
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
130          135          140
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145          150          155          160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
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32

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<400> 41
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 <223> Oligonucleotide primer ZC28345

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<400> 43
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<210> 44

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<223> Oligonucleotide primer ZC976

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